

1652

RAW SEQUENCE LISTING

DATE: 08/14/2000

PATENT APPLICATION: US/09/463,705

TIME: 15:56:17

Input Set : A:\146.1335.txt

Output Set: N:\CRF3\08142000\I463705.raw

Collected Diskette Needed Does Not Comply <110> APPLICANT: Cortes, J Fromentin, C Gaisser, S Leadlay, P Mendez, C Michel, J-M Raynal, M-C 10 Salah-Bey, K Salas, J TC 1800 MAIL ROOM <120> TITLE OF INVENTION: BIOSYNTHESIS GENES & TRANSFER OF 6-DESOXY-HEXOSES IN SACCHAROPOLYSPORA ERYTHRAEA AND IN STREPTOMYCES ANTIBIOTICUS AND THEIR USE 17 <130> FILE REFERENCE: 146.1335 <140> CURRENT APPLICATION NUMBER: 09/463705 20 <141> CURRENT FILING DATE: 2000-02-23 22 <150> PRIOR APPLICATION NUMBER: PCT/FR98/01593 23 <151> PRIOR FILING DATE: 1998-07-21 25 <150> PRIOR APPLICATION NUMBER: 98/07411 26 <151> PRIOR FILING DATE: 1988-06-12 28 <150> PRIOR APPLICATION NUMBER: 97/09458 29 <151> PRIOR FILING DATE: 1997-07-25 31 <160> NUMBER OF SEQ ID NOS: 61

## ERRORED SEQUENCES

2689 <210> SEO ID NO: 21 2690 <211> LENGTH: 246 2691 <212> TYPE: PRT

33 <170> SOFTWARE: PatentIn Ver. 2.1

Response for <213> Organism is mondatory, genus/species, unknown, or artificial sequence.

W--> 2692 <213> ORGANISM: 2694 <400> SEQUENCE: 21
2695 Met Arg Ala Asp Thr Glu Pro Thr Thr Gly Tyr Glu Asp Glu Phe Ala # Please cheek enfire
2696 1 5 10 15
2698 Glu Ile Tyr Asp Ala Val Tyr Arg Gly Arg Gly Lys Asp Tyr Ala Gly
2699 20 25 30
2701 Glu Ala Lys Asp Val Ala Asp Leu Val Arg Asp Arg Val Pro Asp Ala
2702 35 40 45
2704 Ser Ser Leu Leu Asp Val Ala Cys Gly Thr Gly Ala His Leu Arg His this error is recurring.
2705 50 55 60
2707 Phe Ala Thr Leu Phe Asp Asp Ala Arg Gly Leu Glu Leu Ser Ala Ser 2707 Phe Ala Thr Leu Phe Asp Asp Ala Arg Gly Leu Glu Leu Ser Ala Ser 2710 Met Leu Asp Ile Ala Arg Ser Arg Met Pro Gly Val Pro Leu His Gln 2713 Gly Asp Met Arg Ser Phe Asp Leu Gly Pro Arg Val Ser Ala Val Thr 105 2716 Cys Met Phe Ser Ser Val Gly His Leu Ala Thr Thr Ala Glu Leu Asp

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														<b>-</b>						. /
	2717			115					120					125					<i>L</i>	1 00
	2719	Ala	Thr	Leu	Arg	Cys	Phe	Ala	Arg	His	Thr	Arg	Pro	Gly	Gly	Val	Ala		$T_{\alpha}$	r her
	2720		130					135					140				,	000	alla	
	2721	Ile	Glu	Pro	Trp	Trp	Phe	Pro	Glu	Thr	Phe	Thr	Asp	Gly	Tyr	Va /	)	> 6.6	•	ched
E>	2722				-	-	150					155		-	•	V	160			
	2724	Ala	Gly	Asp	Ile	Val	Arg	Val	Asp	Gly	Arg	Thr	Ile	Ser	Arg	Val	Ser	pag	ΘS.	
E>	2725		-	-		165				-	170					175		Pag	• •	
	2727	His	Ser	Val	Arg	Asp	Gly	Gly	Ala	Thr	Arg	Met	Glu	Ile	His	Tyr	Val	, ,		
E>	2728				180					185					190					
	2730	Ile	Ala	Asp	Ala	Glu	His	Gly	Pro	Arg	His	Leu	Val	Glu	His	His	Arg			
E>	2731			195					200					205						
	2733	Ile	Thr	Leu	Phe	Pro	Arg	His	Ala	Tyr	Thr	Ala	Ala	Tyr	Glu	Lys	Ala			
E>	2734		210					215					220							
	2736	Gly	Tyr	Thr	Val	Glu	Tyr	Leu	Asp	Gly	Gly	Pro	Ser	Gly	Arg	Gly	Leu			
E>	2737	225	-				230					235					240			
	2739	Phe	Val	Gly	Thr	Arg	Thr													
E>	2740					245														

09/463,705

## Sequence #20

<400> 20 atq cgq qct qac acq gag ccq acc acc ggg tac gag gac gag ttc qcc 48 Met Arg Ala Asp Thr Glu Pro Thr Thr Gly Tyr Glu Asp Glu Phe Ala gag atc tac gac gcc gtg tac cgg ggc cgg ggc aag gac tac gcc ggc 96 Glu Ile Tyr Asp Ala Val Tyr Arg Gly Arg Gly Lys Asp Tyr Ala Gly gag gcg aag gac gtg gcg gac ctc gtg cgc gac cgg gtg ccg gac gcg 144 Glu Ala Lys Asp Val Ala Asp Leu Val Arg Asp Arg Val Pro Asp Ala tee tee etc etg gae gtg gee tge gge aeg geg eae etg egg eae 192 Ser Ser Leu Leu Asp Val Ala Cys Gly Thr Gly Ala His Leu Arg His ttc qcc acq ctc ttc gac gcc cgc ggt ctc gaa ctg tcc gcg agc 240 Phe Ala Thr Leu Phe Asp Asp Ala Arg Gly Leu Glu Leu Ser Ala Ser atg ctg gac atc gcc cgc tcc cgc atg ccg ggc gtg ccg ctg cac caa 288 Met Leu Asp Ile Ala Arg Ser Arg Met Pro Gly Val Pro Leu His Gln ggg gac atg cga tcc ttc gac ctg ggg cca cgc gtc tcc gcg gtc acc 336 Gly Asp Met Arg Ser Phe Asp Leu Gly Pro Arg Val Ser Ala Val Thr 100 tgc atg ttc agc tcc gtc ggc cac ctg gcc acc gcc gaa ctc gac 384 Cys Met Phe Ser Ser Val Gly His Leu Ala Thr Thr Ala Glu Leu Asp 115 geg acg etg egg tge tte gee egg eac ace egg eec gge gge gtg gee 432 Ala Thr Leu Arg Cys Phe Ala Arg His Thr Arg Pro Gly Gly Val Ala 135 480 gtc atc gaa ccg tgg tgg ttc ccg gag acc ttc acc gac ggc tac gtg (Val)\Ile Glu Pro Trp Trp Phe Pro Glu Thr Phe Thr Asp Gly Tyr Val In sequence #21 following, it appears that this porticular Valine residue was somehow deleted, thus causing errors in the amino acid numbering

region, and an invalid amino count. (245 instrad of 246)

<210> 21 <211> 246 <212> PRT <213>

Sequence #21

<400> 21

Met Arg Ala Asp Thr Glu Pro Thr Thr Gly Tyr Glu Asp Glu Phe Ala  $1 \hspace{1cm} 5 \hspace{1cm} 10 \hspace{1cm} 15$ 

Glu Ile Tyr Asp Ala Val Tyr Arg Gly Arg Gly Lys Asp Tyr Ala Gly
20 25 30

Glu Ala Lys Asp Val Ala Asp Leu Val Arg Asp Arg Val Pro Asp Ala 35 40 45

Ser Ser Leu Leu Asp Val Ala Cys Gly Thr Gly Ala His Leu Arg His 50 55 60

Phe Ala Thr Leu Phe Asp Asp Ala Arg Gly Leu Glu Leu Ser Ala Ser 65 70 75 80

Met Leu Asp Ile Ala Arg Ser Arg Met Pro Gly Val Pro Leu His Gln 85 90 · 95

Gly Asp Met Arg Ser Phe Asp Leu Gly Pro Arg Val Ser Ala Val Thr 100 105 110

Cys Met Phe Ser Ser Val Gly His Leu Ala Thr Thr Ala Glu Leu Asp 115 120 125

Ala Thr Leu Arg Cys Phe Ala Arg His Thr Arg Pro Gly Gly Val Ala
130
135
140
11e Glu Pro Trp Trp Phe Pro Glu Thr Phe Thr Asp Gly Tyr Val
155
160

here would correct the error. No adjustment to the numbering sequence is required.

VERIFICATION SUMMARY

DATE: 08/14/2000 TIME: 15:56:18

PATENT APPLICATION: US/09/463,705

input Set : A:\146.1335.txt

L:868 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:6

Output Set: N:\CRF3\08142000\I463705.raw

L:42 M:351 W: Sequence data Name/Key Feature Out-of-Range, SEQ ID#:1, CDS LOCATION: Complement((48)... (1046)) L:48 M:351 W: Sequence data Name/Key Feature Out-of-Range, SEQ ID#:1, CDS LOCATION: Complement((2322)... (3404)) L:173 M:201 W: Mandatory field data missing, ORGANISM L:243 M:201 W: Mandatory field data missing, ORGANISM L:324 M:351 W: Sequence data Name/Key Feature Out-of-Range, SEQ ID#:4, CDS LOCATION: complement (4)..(1266) L:378 M:201 W: Mandatory field data missing, ORGANISM L:603 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ:ID:6 L:607 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:6 L:710 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:6 L:714 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:6 L:718 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:6 L:722 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:6 L:726 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:6 L:730 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:6 L:734 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:6 L:738 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:6 L:742 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:6 L:746 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:6 L:750 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:6 L:754 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:6 L:758 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:6 L:762 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:6 L:766 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:6 L:772 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:6 L:776 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:6 L:780 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:6 L:784 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:6 L:788 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:6 L:792 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:6 L:796 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:6 L:800 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:6 L:804 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:6 L:808 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:6 L:812 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:6 L:816 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:6 L:820 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:6 L:824 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:6 L:828 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:6 L:832 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:6 L:836 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:6 L:840 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:6 L:844 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:6 L:848 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:6 L:852 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:6 L:856 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:6 L:860 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:6 L:864 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:6

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Input Set : A:\146.1335.txt

Output Set: N:\CRF3\08142000\I463705.raw '

```
L:872 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:6 .
L:876 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:6
L:880 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:6
L:884 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:6
L:888 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:6
L:892 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:6
L:896 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:6
L:900 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:6
L:1122 M:201 W: Mandatory field data missing, ORGANISM
L:1191 M:201 W: Mandatory field data missing, ORGANISM
L:1276 M:201 W: Mandatory field data missing, ORGANISM
L:1328 M:201 W: Mandatory field data missing, ORGANISM
L:1430 M:201 W: Mandatory field data missing, ORGANISM
L:1530 M:201 W: Mandatory field data missing, ORGANISM
L:1696 M:201 W: Mandatory field data missing, ORGANISM L:2269 M:201 W: Mandatory field data missing, ORGANISM
L:2353 M:201 W: Mandatory field data missing, ORGANISM L:2441 M:201 W: Mandatory field data missing, ORGANISM
L:2529 M:201 W: Mandatory field data missing, ORGANISM
L:2692 M:201 W: Mandatory field data missing, ORGANISM
L:2722 M:332 E: (32) Invalid/Missing Amino Acid Numbering, SEQ ID:21
M:332 Repeated in SeqNo=21
L:2740 M:252 E: No. of Seq. differs, <211>LENGTH:Input:246 Found:245 SEQ:21
L:2746 M:201 W: Mandatory field data missing, ORGANISM L:2758 M:201 W: Mandatory field data missing, ORGANISM
L:2770 M:201 W: Mandatory field data missing, ORGANISM L:2782 M:201 W: Mandatory field data missing, ORGANISM
L:2806\ M:201\ W: Mandatory field data missing, ORGANISM
L:2818 M:201 W: Mandatory field data missing, ORGANISM
L:2830 M:201 W: Mandatory field data missing, ORGANISM
L:2842 M:201 W: Mandatory field data missing, ORGANISM
L:2854 M:201 W: Mandatory field data missing, ORGANISM
L:2866 M:201 W: Mandatory field data missing, ORGANISM
L:2878 M:201 W: Mandatory field data missing, ORGANISM
L:2890 M:201 W: Mandatory field data missing, ORGANISM
L:2902 M:201 W: Mandatory field data missing, ORGANISM
L:2914 M:201 W: Mandatory field data missing, ORGANISM L:2926 M:201 W: Mandatory field data missing, ORGANISM
L:2938 M:201 W: Mandatory field data missing, ORGANISM L:2950 M:201 W: Mandatory field data missing, ORGANISM
L:2962\ M:201\ W: Mandatory field data missing, ORGANISM
L:2974 M:201 W: Mandatory field data missing, ORGANISM
L:2986 M:201 W: Mandatory field data missing, ORGANISM
L:2998 M:201 W: Mandatory field data missing, ORGANISM
L:3010 M:201 W: Mandatory field data missing, ORGANISM
L:3022 M:201 W: Mandatory field data missing, ORGANISM
L:3036 M:201 W: Mandatory field data missing, ORGANISM
L:3048 M:201 W: Mandatory field data missing, ORGANISM
L:3060 M:201 W: Mandatory field data missing, ORGANISM
```

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Output Set: N:\CRF3\08142000\1463705.raw

			Mandatory					
L:3086	M:201	₩:	Mandatory	field	data	missing,	ORGANISM	
L:3098	M:201	₩:	Mandatory	field	data	missing,	ORGANISM	
L:3110	M:201	W:	Mandatory	field	data	missing,	ORGANISM	
L:3122	M:201	W:	Mandatory	field.	data	missing,	ORGANISM	
L:3134	M:201	W:	Mandatory	field	data	missing,	ORGANISM	
L:3146	M:201	W:	Mandatory	field	data	missing,	ORGANISM	
L:3158	M:201	W:	Mandatory	field	data	missing,	ORGANISM	
L:3170	M:201	W:	Mandatory	field	data	missing,	ORGANISM	